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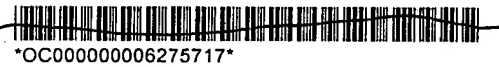
APPLICATION NUMBER	FILING/RECEIPT DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NUMBER
09/709,905	11/10/2000	Kalyanaraman Ramnarayan	24737-1906C

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HELLER EHRMAN WHITE & MCAULIFFE LLP  
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SAN DIEGO, CA 92122-1246



CONFIRMATION NO. 3606

FORMALITIES LETTER



Date Mailed: 07/10/2001

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS  
CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE  
DISCLOSURES**

Applicant is given **TWO MONTHS FROM THE DATE OF THIS NOTICE** within which to file the items indicated below to avoid abandonment. Extensions of time may be obtained under the provisions of 37 CFR 1.136(a).

- A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing." Applicant must provide a substitute computer readable form (CRF) copy of the "Sequence Listing" and a statement that the content of the sequence listing information recorded in computer readable form is identical to the written (on paper or compact disc) sequence listing and, where applicable, includes no new matter, as required by 37 CFR 1.821(e), 1.821(f), 1.821(g), 1.825(b), or 1.825(d).

For questions regarding compliance to these requirements, please contact:

- For Rules Interpretation, call (703) 308-4216
- To Purchase PatentIn Software, call (703) 306-2600
- For PatentIn Software Program Help, call (703) 306-4119 or e-mail at [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or [patin3help@uspto.gov](mailto:patin3help@uspto.gov)

*A copy of this notice **MUST** be returned with the reply.*

Customer Service Center  
Initial Patent Examination Division (703) 308-1202

PART 2 - COPY TO BE RETURNED WITH RESPONSE

# RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY  
SYSTEMS  
BRANCH

SEP 04 2001

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/709,905

Source: OIPE

Date Processed by STIC: 3/13/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER: 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX: 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER  
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE. SEE BELOW.

## Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST-25. Checker Version 3.0 replaces the previous DOS-based version of Checker and is Y2K compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be downloaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>



OIPE

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/709,905

DATE: 03/13/2001  
TIME: 15:05:04

Input Set : A:\1906cseq.002  
Output Set: N:\CRF3\03132001\I709905.raw

4 <110> APPLICANT: Kalyanaraman Ramnarayan  
5 Edward T. Maggio  
6 P. Patrick Hess  
9 <120> TITLE OF INVENTION: Use of Computationally Derived Protein  
10 Structures of Genetic Polymorphisms in Pharmacogenomics for  
11 Drug Design and Clinical Applications  
15 <130> FILE REFERENCE: 24737-1906C  
\* 17 <140> CURRENT APPLICATION NUMBER: US/09/709,905  
18 <141> CURRENT FILING DATE: 2000-11-10  
20 <150> PRIOR APPLICATION NUMBER: 09/438,566  
21 <151> PRIOR FILING DATE: 1999-11-10  
23 <150> PRIOR APPLICATION NUMBER: 24737-1906B  
24 <151> PRIOR FILING DATE: 2000-11-01  
26 <160> NUMBER OF SEQ ID NOS: 118  
28 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
30 <210> SEQ ID NO: 1  
31 <211> LENGTH: 6  
32 <212> TYPE: PRT  
33 <213> ORGANISM: Artificial Sequence  
35 <220> FEATURE:  
36 <223> OTHER INFORMATION: Modified Hepatitis C Virus NS3 Protease Inhibitor  
37 Peptide  
40 <221> NAME/KEY: ACETYLTATION  
41 <222> LOCATION: 1  
43 <221> NAME/KEY: MOD\_RES  
44 <222> LOCATION: 2  
45 <223> OTHER INFORMATION: D-glutamic acid  
47 <221> NAME/KEY: MOD\_RES  
48 <222> LOCATION: 5  
49 <223> OTHER INFORMATION: beta-cyclohexylalanine  
51 <300> PUBLICATION INFORMATION:  
52 <301> AUTHORS: Ingallinella, P., Altamura, S., Bianchi, E., Talia  
53 <302> TITLE: Potent Peptide Inhibitors Of Human Hepatitis C Vir  
54 <303> JOURNAL: Biochemistry  
55 <304> VOLUME: 37  
56 <305> ISSUE: 25  
57 <306> PAGES: 8906-8914  
58 <307> DATE: 1998-06-23  
OK 60 <400> SEQUENCE: 1  
61 Asp Xaa Leu Ile Xaa Cys  
62 1 5  
64 <210> SEQ ID NO: 2  
65 <211> LENGTH: 6  
66 <212> TYPE: PRT  
67 <213> ORGANISM: Artificial Sequence  
69 <220> FEATURE:  
70 <223> OTHER INFORMATION: Modified Hepatitis C Virus NS3 Protease Inhibitor

ppr. 2, 4-5  
Does Not Comply  
Corrected Diskette Needed

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/709,905  
 DATE: 03/13/2001  
 TIME: 15:05:04

Input Set : A:\1906cseq.002  
 Output Set: N:\CRF3\03132001\1709905.raw

71 Peptide  
 75 <221> NAME/KEY: ACETYLTATION  
 76 <222> LOCATION: 1  
 78 <221> NAME/KEY: MOD\_RES  
 79 <222> LOCATION: 5  
 80 <223> OTHER INFORMATION: beta-cyclohexylalanine  
 82 <300> PUBLICATION INFORMATION:  
 83 <301> AUTHORS: Ingallinella, P., Altamura, S., Bianchi, E., Talia  
 84 <302> TITLE: Potent Peptide Inhibitors Of Human Hepatitis C Vir  
 85 <303> JOURNAL: Biochemistry  
 86 <304> VOLUME: 37  
 87 <305> ISSUE: 25  
 88 <306> PAGES: 8906-8914  
 89 <307> DATE: 1998-06-23  
 91 <400> SEQUENCE: 2  
 OK> 92 Asp Glu Leu Ile Xaa Cys  
 93 1 5  
 95 <210> SEQ ID NO: 3  
 96 <211> LENGTH: 1045  
 97 <212> TYPE: DNA  
 98 <213> ORGANISM: Human Immunodeficiency Virus (HIV)  
 100 <220> FEATURE:  
 101 <221> NAME/KEY: CDS  
 W--> 102 <222> LOCATION: (0)..  
 103 <223> OTHER INFORMATION: Protease  
 105 <221> NAME/KEY: CDS  
 OK> 106 <222> LOCATION: (298)...(1045)  
 107 <223> OTHER INFORMATION: Portion of Reverse Transcriptase  
 109 <400> SEQUENCE: 3  
 110 cct cag atc act ctt tgg caa cga ccc cty gtc aca ata aag ata ggg 48  
 W--> 111 Pro Gln Ile Thr Leu Trp Gln Arg Pro Xaa Val Thr Ile Lys Ile Gly  
 112 1 5 10 15  
 114 ggc caa cta aaa gaa gct yta tta gat aca gga gca gat gat aca gta 96  
 115 Gly Gln Leu Lys Glu Ala Xaa Leu Asp Thr Gly Ala Asp Asp Thr Val  
 116 20 25 30  
 118 tta gaa gaa atg agt tta cca ggg aaa tgg aaa cca aaa atg ata ggg 144  
 119 Leu Glu Glu Met Ser Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly  
 120 35 40 45  
 122 gga att gga ggt ttt atc aaa gta aga cag tat gat caa ala ctc ata 192  
 123 Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Leu Ile  
 124 50 55 60  
 126 gaa atc tgt gga cat aaa gct ata ggc aca gta tta gta gga cct aca 240  
 127 Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr  
 128 65 70 75 80  
 130 cct gtc aac ata att gga aga aat ttg ttg act cag att ggt tgc act 288  
 131 Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr  
 132 85 90 95  
 134 tta aat ttg ccc att agt cct att gaa act gta cca gta aaa tta aag 336  
 135 Leu Asn Leu Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys

*(global error)*  
*(1) ← coding begins at first base (global error)*

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/709,905

DATE: 03/13/2001

TIME: 15:05:04

Input Set : A:\1906cseq.002

Output Set: N:\CRF3\03132001\I709905.raw

136 100 105 110  
 138 cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384  
 139 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu  
 140 115 120 125  
 142 aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa gga 432  
 143 Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly  
 144 130 135 140  
 146 aaa att tca aaa att ggg cct gag aat cca tac aat act cca ata ttt 480  
 147 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe  
 148 145 150 155 160  
 150 gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc 528  
 151 Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe  
 152 165 170 175  
 154 aga gaa ctt aat aag aga aca caa gac ttc tgg gaa gtt caa tta gga 576  
 155 Arg Glu Leu Asn Lys Arg Thr Glu Asp Phe Trp Glu Val Gln Leu Gly  
 156 180 185 190  
 158 ata cca cac ccc gca ggg tta aaa cag aaa aaa tca gta aca ata ctg 624  
 159 Ile Pro His Pro Ala Gly Leu Lys Gln Lys Lys Ser Val Thr Ile Leu  
 160 195 200 205  
 162 gat gtg ggt gat gca tat ttt tca gtt ccc tta gat gaa ggc ttc agg 672  
 163 Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Gly Phe Arg  
 164 210 215 220  
 166 aag tat act gca ttt acc ata cct agt aga aat aat gag aca cca ggg 720  
 167 Lys Tyr Thr Ala Phe Thr Ile Pro Ser Arg Asn Asn Glu Thr Pro Gly  
 168 225 230 235 240  
 170 att aga tat cag tac aac gtg ctc cca cag gga tgg aaa gga tca cca 768  
 171 Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro  
 172 245 250 255  
 174 gca ata ttt caa agt agc atg aca aga aty tta gag cct ttt aga aaa 816  
 175 Ala Ile Phe Gln Ser Ser Met Thr Arg Xaa Leu Glu Pro Phe Arg Lys  
 176 260 265 270  
 178 caa aat cca gaa ata gtt atc tat caa tac atg gat gat ttg tat gta 864  
 179 Gln Asn Pro Glu Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val  
 180 275 280 285  
 182 gga tct gac tta gaa ata gga cag cat aga gca aaa ata gag gaa ctg 912  
 183 Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Gln Glu Leu  
 184 290 295 300  
 186 aga gga cat cta tta aag tgg gga ttt acc aca cca gac aaa aaa cat 960  
 187 Arg Gly His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His  
 188 305 310 315 320  
 190 cag aaa gaa cct cca ttt ctt tgg atg ggt tat gaa ctc cat cct gat 1008  
 191 Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp  
 192 325 330 335  
 194 aaa tgg aca gta cag cct ata aag ttg cca gaa aaa g 1045  
 195 Lys Trp Thr Val Gln Pro Ile Lys Leu Pro Glu Lys  
 196 340 345  
 199 <210> SEQ ID NO: 4  
 200 <211> LENGTH: 1046  
 201 <212> TYPE: DNA

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/709,905

DATE: 03/13/2001

TIME: 15:05:04

Input Set : A:\1906cseq.002

Output Set: N:\CRF3\03132001\I709905.raw

202 <213> ORGANISM: Human Immunodeficiency Virus (HIV)  
 204 <220> FEATURE:  
 205 <221> NAME/KEY: CDS (1) ←  
 W--> 206 <222> LOCATION: (10)...(297)  
 207 <223> OTHER INFORMATION: HIV Protease  
 209 <221> NAME/KEY: CDS  
 210 <222> LOCATION: (298)...(1046)  
 211 <223> OTHER INFORMATION: Portion of HIV Reverse Transcriptase  
 213 <400> SEQUENCE: 4  
 214 cct cag atc act ctt tgg caa cga ccc ctt gtc aca ata aag ata gga 48  
 215 Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly  
 216 1 5 10 15  
 218 ggg cag cta aag gaa gct cta tta gat aca gga gca gat gat aca gta 96  
 219 Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val  
 220 20 25 30  
 222 gtt gaa gaa atg aat ttg cca gga aaa tgg aaa cca aaa atg ata ggg 144  
 223 Val Glu Glu Met Asn Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly  
 224 35 40 45  
 226 gga att gga ggt ttt atc aaa gta aga cag tat gag caa ata gcc gta 192  
 227 Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Glu Gln Ile Ala Val  
 228 50 55 60  
 230 gaa aty tgt gga cat aga gct atg ggt aca gta tta gta gga cct aca 240  
 231 Glu Xaa Cys Gly His Arg Ala Met Gly Thr Val Leu Val Gly Pro Thr  
 232 65 70 75 80  
 234 ccg gtc aac ata att gga aga aat ctg ttg act cag att ggt tgc act 288  
 235 Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr  
 236 85 90 95  
 238 tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336  
 239 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys  
 240 100 105 110  
 242 cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384  
 243 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu  
 244 115 120 125  
 246 aaa ata aaa gca tta gta gaa atc tgt aca gaa ttg gaa aag gaa ggg 432  
 247 Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly  
 248 130 135 140  
 250 aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt 480  
 251 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe  
 252 145 150 155 160  
 254 gcc ata aag aaa aag aac agt act aaa tgg aga aaa tta gta gat ttc 528  
 255 Ala Ile Lys Lys Lys Asn Ser Thr Lys Trp Arg Lys Leu Val Asp Phe  
 256 165 170 175  
 258 aga gaa ctt aat aag aga act caa gac ttc tgg gag gtt caa tta gga 576  
 259 Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly  
 260 180 185 190  
 262 ata cca cat cca gca ggg tta aaa aag aat aaa tca ata aca gta ctg 624  
 263 Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Ile Thr Val Leu  
 264 195 200 205  
 266 gat gtg ggt gat gca tat ttt tca gtt ccc tta tgr gaa gac ttc agg 672

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/709,905

DATE: 03/13/2001

TIME: 15:05:04

Input Set : A:\1906cseq.002

Output Set: N:\CRF3\03132001\I709905.raw

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267 Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Cys Glu Asp Phe Arg
268      210      215      220
270 aag tat act gca ttt acc ata cct agt gta aac aat gag act cca ggg      720
271 Lys Tyr Thr Ala Phe Thr Ile Pro Ser Val Asn Asn Glu Thr Pro Gly
272 225      230      235      240
274 att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga ttc acc      768
275 ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Phe Thr
276      245      250      255
278 agc ata ttc caa tgt agc atg aca aaa atc tta gag cct ttt aga aaa      816
279 Ser Ile Phe Gln Cys Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys
280      260      265      270
282 caa aat cca gag ata gtt atc tat caa tac atg gat gat ttg tat gta      864
283 Gln Asn Pro Glu Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val
284      275      280      285
286 gga tct gac tta gaa ata ggg cag cat aga gca aaa ata gag gaa ctg      912
287 Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Glu Leu
288      290      295      300
290 aga caa tat ctg tgg aag tgg gga ttt tgc aca cca gaa caa aar cat      960
291 Arg Gln Tyr Leu Trp Lys Trp Gly Phe Cys Thr Pro Glu Gln Lys His
292 305      310      315      320
294 cag aaa gaa cct cct ttc ctt tgg atg ggt tat gaa ctc cat ccc gat      1008
295 Gln Lys Gln Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
296      325      330      335
298 aaa tgg aca gta caa cct ata gtg ctg cca gac aaa ga      1046
299 Lys Trp Thr Val Gln Pro Ile Val Leu Pro Asp Lys
300      340      345
303 <210> SEQ ID NO: 5
304 <211> LENGTH: 1104
305 <212> TYPE: DNA
306 <213> ORGANISM: Human Immunodeficiency Virus (HIV)
308 <220> FEATURE:
309 <221> NAME/KEY: CDS (1)
W--> 310 <222> LOCATION: (0)...(297)
311 <223> OTHER INFORMATION: HIV Protease
313 <221> NAME/KEY: CDS
314 <222> LOCATION: (298)...(1104)
315 <223> OTHER INFORMATION: Portion of HIV Reverse Transcriptase
317 <400> SEQUENCE: 5
318 cct cag atc act ctt tgg caa cga ccc atc gtc aca ata aag rta ggg      48
319 Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Ile Lys Xaa Gly
320 1      5      10      15
322 ggg caa cta agg gaa gct cta tta gat aca gga gca gat gat aca ata      96
323 Gly Gln Leu Arg Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Ile
324      20      25      30
326 ata gaa gac ata act ttg cca gga aga tgg aca cca aaa atg ata ggg      144
327 Ile Glu Asp Ile Thr Leu Pro Gly Arg Trp Thr Pro Lys Met Ile Gly
328      35      40      45
330 gga att gga ggt ttt gtc aaa gta aga cag tat gat cag ata ccc ata      192
331 Gly Ile Gly Gly Phe Val Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile

```

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

FYI:

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/709,905

DATE: 03/13/2001

TIME: 15:05:05

Input Set : A:\1906cseq.002

Output Set: N:\CRF3\03132001\I709905.raw

L:17 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:61 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:92 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:102 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:3, CDS LOCATION: (0)...(297)  
L:111 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:115 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:175 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:206 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:4, CDS LOCATION: (0)...(297)  
L:231 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:310 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:5, CDS LOCATION: (0)...(297)  
L:319 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:335 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:351 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:418 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:6, CDS LOCATION: (0)...(297)  
L:530 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:7, CDS LOCATION: (0)...(297)  
L:546 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:547 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:555 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:642 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:8, CDS LOCATION: (0)...(297)  
L:651 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:655 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:754 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:9, CDS LOCATION: (0)...(297)  
L:763 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:783 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:835 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:843 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:866 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:10, CDS LOCATION: (0)...(297)  
L:879 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10  
L:883 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10  
L:935 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10  
L:943 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10  
L:978 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:11, CDS LOCATION: (0)...(297)  
L:987 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11  
L:991 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11  
L:1011 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11  
L:1059 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11  
L:1090 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:12, CDS LOCATION: (0)...(297)  
L:1171 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:1202 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:13, CDS LOCATION: (0)...(297)  
L:1211 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13  
L:1215 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13  
L:1259 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13  
L:1279 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13  
L:1314 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:14, CDS LOCATION: (0)...(297)  
L:1387 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14  
L:1395 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14  
L:1399 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14  
L:1426 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:15, CDS LOCATION: (0)...(297)



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L:1443 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15  
 L:1447 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15  
 L:1499 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15  
 L:1515 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15  
 L:1523 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15  
 L:1538 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:16, CDS LOCATION: (0)...(297)  
 L:1579 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16  
 L:1619 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16  
 L:1650 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:17, CDS LOCATION: (0)...(297)  
 L:1659 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
 L:1671 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
 L:1715 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
 L:1719 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
 L:1735 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
 L:1739 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
 L:1750 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
 L:1762 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:18, CDS LOCATION: (0)...(297)  
 L:1783 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
 L:1819 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
 L:1874 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:19, CDS LOCATION: (0)...(297)  
 L:1986 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:20, CDS LOCATION: (0)...(297)  
 L:2098 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:21, CDS LOCATION: (0)...(297)  
 L:2210 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:22, CDS LOCATION: (0)...(297)  
 L:2322 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:23, CDS LOCATION: (0)...(297)  
 L:2434 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:24, CDS LOCATION: (0)...(297)  
 L:2546 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:25, CDS LOCATION: (0)...(297)  
 L:2658 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:26, CDS LOCATION: (0)...(297)  
 L:2770 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:27, CDS LOCATION: (0)...(297)  
 L:2774 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:27, CDS LOCATION: (298)...(1116)  
 L:2882 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:28, CDS LOCATION: (0)...(297)  
 L:2994 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:29, CDS LOCATION: (0)...(297)  
 L:3106 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:30, CDS LOCATION: (0)...(297)  
 L:3218 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:31, CDS LOCATION: (0)...(297)  
 L:3330 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:32, CDS LOCATION: (0)...(297)  
 L:3442 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:33, CDS LOCATION: (0)...(297)  
 L:3554 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:34, CDS LOCATION: (0)...(297)  
 L:3666 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:35, CDS LOCATION: (0)...(297)  
 L:3778 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:36, CDS LOCATION: (0)...(297)  
 L:3890 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:37, CDS LOCATION: (0)...(297)  
 L:4002 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:38, CDS LOCATION: (0)...(297)  
 L:4114 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:39, CDS LOCATION: (0)...(297)  
 L:4226 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:40, CDS LOCATION: (0)...(297)  
 L:4338 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:41, CDS LOCATION: (0)...(297)  
 L:4446 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:42, CDS LOCATION: (0)...(297)  
 L:4550 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:43, CDS LOCATION: (0)...(297)  
 L:4658 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:44, CDS LOCATION: (0)...(297)  
 L:4770 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:45, CDS LOCATION: (0)...(297)  
 L:4882 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:46, CDS LOCATION: (0)...(297)  
 L:4994 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:47, CDS LOCATION: (0)...(297)

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L:5106 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:48, CDS LOCATION: (0)...(297)  
L:5218 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:49, CDS LOCATION: (0)...(297)  
L:5330 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:50, CDS LOCATION: (0)...(297)  
L:5442 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:51, CDS LOCATION: (0)...(297)